

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/198,723ADATE: 04/16/1999
TIME: 14:06:48

INPUT SET: S31474.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Malcolm, Bruce
6 Taremi, Shahriar S.
7 Weber, Patricia
8 Yao, Nanhua
9
10 (ii) TITLE OF INVENTION: Covalent Complexes of Hepatitis C Virus
11 NS3 Protease and NS4A Cofactor Peptide
12
13 (iii) NUMBER OF SEQUENCES: 123
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Schering-Plough Corp.
17 (B) STREET: 2000 Galloping Hill Road
18 (C) CITY: Kenilworth
19 (D) STATE: New Jersey
20 (E) COUNTRY: USA
21 (F) ZIP: 07030
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: Power Macintosh
26 (C) OPERATING SYSTEM: 8.0.1
27 (D) SOFTWARE: Microsoft Word 6.0.1
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: US 09/198,723
31 (B) FILING DATE: 24 NOV 1998
32 (C) CLASSIFICATION:
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: McLaughlin, Jaye P.
36 (B) REGISTRATION NUMBER: 41,211
37 (C) REFERENCE/DOCKET NUMBER: JB0800
38
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: (908)298-5056
41 (B) TELEFAX: (908)298-5388
42
43
44
45
46

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/198,723ADATE: 04/16/1999
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INPUT SET: S31474.raw

47 (2) INFORMATION FOR SEQ ID NO:1:

48

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 216 amino acids

51 (B) TYPE: amino acid

52 (D) TOPOLOGY: linear

53

54 (ii) MOLECULE TYPE: protein

55

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

57

58 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

59 1 5 10 15

60

61 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu

62 20 25 30

63

64 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu

65 35 40 45

66

67 Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val

68 50 55 60

69

70 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala

71 65 70 75 80

72

73 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser

74 85 90 95

75

76 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn

77 100 105 110

78

79 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser

80 115 120 125

81

82 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg

83 130 135 140

84

85 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser

86 145 150 155 160

87

88 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly

89 165 170 175

90

91 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala

92 180 185 190

93

94 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu

95 195 200 205

96

97 Ser Met Glu Thr Thr Met Arg Ser

98 210 215

99

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100

101

102

103 (2) INFORMATION FOR SEQ ID NO:2:

104

105 (i) SEQUENCE CHARACTERISTICS:

106 (A) LENGTH: 216 amino acids

107 (B) TYPE: amino acid

108 (D) TOPOLOGY: linear

109

110 (ii) MOLECULE TYPE: protein

111

112 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

113

114 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro

115 1 5 10 15

116

117 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu

118 20 25 30

119

120 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu

121 35 40 45

122

123 Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val

124 50 55 60

125

126 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala

127 65 70 75 80

128

129 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser

130 85 90 95

131

132 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn

133 100 105 110

134

135 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser

136 115 120 125

137

138 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg

139 130 135 140

140

141 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser

142 145 150 155 160

143

144 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly

145 165 170 175

146

147 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala

148 180 185 190

149

150 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu

151 195 200 205

152

RAW SEQUENCE LISTING

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153 Ser Met Glu Thr Thr Met Arg Ser
154 210 215
155
156
157
158

159 (2) INFORMATION FOR SEQ ID NO:3:
160

161 (i) SEQUENCE CHARACTERISTICS:
162 (A) LENGTH: 216 amino acids
163 (B) TYPE: amino acid
164 (D) TOPOLOGY: linear
165

166 (ii) MOLECULE TYPE: protein
167

168 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
169

170 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
171 1 5 10 15
172

173 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
174 20 25 30
175

176 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
177 35 40 45
178

179 Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
180 50 55 60
181

182 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
183 65 70 75 80
184

185 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
186 85 90 95
187

188 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
189 100 105 110
190

191 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
192 115 120 125
193

194 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
195 130 135 140
196

197 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
198 145 150 155 160
199

200 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly
201 165 170 175
202

203 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
204 180 185 190
205

RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

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```

206 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
207      195                      200                      205
208
209 Ser Met Glu Thr Thr Met Arg Ser
210      210                      215
211
212
213
214
215 (2) INFORMATION FOR SEQ ID NO:4:
216
217     (i) SEQUENCE CHARACTERISTICS:
218         (A) LENGTH: 216 amino acids
219         (B) TYPE: amino acid
220         (D) TOPOLOGY: linear
221
222     (ii) MOLECULE TYPE: protein
223
224     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
225
226 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
227   1                      5                      10                      15
228
229 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
230      20                      25                      30
231
232 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
233      35                      40                      45
234
235 Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
236      50                      55                      60
237
238 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
239      65                      70                      75                      80
240
241 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
242      85                      90                      95
243
244 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
245      100                     105                     110
246
247 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
248      115                     120                     125
249
250 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
251      130                     135                     140
252
253 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
254      145                     150                     155                     160
255
256 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly
257      165                     170                     175
258

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

DATE: 04/16/1999
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***** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

4116 (2) INFORMATION FOR SEQ ID NO:92:

4117

4118 (i) SEQUENCE CHARACTERISTICS:

4119 (A) LENGTH: 651 base pairs

4120 (B) TYPE: nucleic acid

4121 (C) STRANDEDNESS: single

4122 (D) TOPOLOGY: linear

4123

4124 (ii) MOLECULE TYPE: cDNA

4125

4126

4127

4128 (ix) FEATURE:

4129 (A) NAME/KEY: CDS

4130 (B) LOCATION: 1..651

4131

4132

4133 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

4134

4135 ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48

4136 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro

4137 1 5 10 15

4138

4139 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96

4140 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu

4141 20 25 30

4142

4143 TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA 144

4144 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu

4145 35 40 45

4146

4147 CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC 192

4148 Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val

4149 50 55 60

4150

4151 GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG 240

4152 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala

4153 65 70 75 80

4154

4155 ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA 288

4156 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser

4157 85 90 95

4158

4159 AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT 336

4160 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn

4161 100 105 110

4162

RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

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4163	GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
4164	Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
4165	115 120 125	
4166		
4167	TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
4168	Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
4169	130 135 140	
4170		
4171	CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
4172	His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
4173	145 150 155 160	
4174		
4175	CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT	528
4176	Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly	
4177	165 170 175	
4178		
4179	CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576
4180	Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	
4181	180 185 190	
4182		
4183	GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG	624
4184	Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	
4185	195 200 205	
4186		
4187	TCC ATG GAA ACT ACT ATG CGG TCT TGA	651
4188	Ser Met Glu Thr Thr Met Arg Ser	
4189	210 215	
4190		
4191		

4869 (2) INFORMATION FOR SEQ ID NO:102:

4870

(i) SEQUENCE CHARACTERISTICS:

4872 (A) LENGTH: 1998 base pairs

4873 (B) TYPE: nucleic acid

4874 (C) STRANDEDNESS: single

4875 (D) TOPOLOGY: linear

4876

4877 (ii) MOLECULE TYPE: cDNA

4878

4879

(ix) FEATURE:

4881 (A) NAME/KEY: CDS

4882 (B) LOCATION: 1..1998

4883

4884

4885 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

4886

4887 ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48

4888 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro

4889 1 5 10 15

4890

4891 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96

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4892	Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
4893	20 25 30	
4894		
4895	TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
4896	Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
4897	35 40 45	
4898		
4899	CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
4900	Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
4901	50 55 60	
4902		
4903	GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
4904	Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
4905	65 70 75 80	
4906		
4907	ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
4908	Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
4909	85 90 95	
4910		
4911	AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
4912	Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
4913	100 105 110	
4914		
4915	GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
4916	Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
4917	115 120 125	
4918		
4919	TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
4920	Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
4921	130 135 140	
4922		
4923	CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
4924	His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
4925	145 150 155 160	
4926		
4927	CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT	528
4928	Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly	
4929	165 170 175	
4930		
4931	CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576
4932	Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	
4933	180 185 190	
4934		
4935	GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG	624
4936	Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	
4937	195 200 205	
4938		
4939	TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC	672
4940	Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser	
4941	210 215 220	
4942		
4943	CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC	720
4944	Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro	

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	225	230	235	240	
4945					
4946					
4947	ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA				768
4948	Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln				
4949		245	250	255	
4950					
4951	GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG				816
4952	Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly				
4953		260	265	270	
4954					
4955	TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA				864
4956	Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg				
4957		275	280	285	
4958					
4959	ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC				912
4960	Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr				
4961		290	295	300	
4962					
4963	TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC				960
4964	Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp				
4965		305	310	315	320
4966					
4967	ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG				1008
4968	Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu				
4969		325	330	335	
4970					
4971	GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT				1056
4972	Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu				
4973		340	345	350	
4974					
4975	GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC				1104
4976	Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His				
4977		355	360	365	
4978					
4979	CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC				1152
4980	Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe				
4981		370	375	380	
4982					
4983	TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC				1200
4984	Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu				
4985		385	390	395	400
4986					
4987	ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG				1248
4988	Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu				
4989		405	410	415	
4990					
4991	TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG				1296
4992	Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val				
4993		420	425	430	
4994					
4995	TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT				1344
4996	Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala				
4997		435	440	445	

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4998																		
4999	CTG	ATG	ACG	GGC	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC		1392
5000	Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn		
5001		450					455					460						
5002																		
5003	ACA	TGT	GTC	ACC	CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC		1440
5004	Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr		
5005	465					470					475					480		
5006																		
5007	ATT	GAG	ACG	ACG	ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG		1488
5008	Ile	Glu	Thr	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg		
5009					485					490					495			
5010																		
5011	CGG	GGT	AGG	ACT	GGC	AGG	GGT	AGG	AGA	GGC	ATC	TAC	AGG	TTT	GTG	ACT		1536
5012	Arg	Gly	Arg	Thr	Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr		
5013				500					505					510				
5014																		
5015	CCG	GGA	GAA	CGG	CCC	TCG	GGC	ATG	TTC	GAT	TCC	TCG	GTC	CTG	TGT	GAG		1584
5016	Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu		
5017			515					520					525					
5018																		
5019	TGC	TAT	GAC	GCG	GGC	TGT	GCT	TGG	TAC	GAG	CTC	ACC	CCC	GCC	GAG	ACC		1632
5020	Cys	Tyr	Asp	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr		
5021		530					535					540						
5022																		
5023	TCG	GTT	AGG	TTG	CGG	GCC	TAC	CTG	AAC	ACA	CCA	GGG	TTG	CCC	GTT	TGC		1680
5024	Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys		
5025	545					550					555					560		
5026																		
5027	CAG	GAC	CAC	CTG	GAG	TTC	TGG	GAG	AGT	GTC	TTC	ACA	GGC	CTC	ACC	CAT		1728
5028	Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His		
5029					565					570					575			
5030																		
5031	ATA	GAT	GCA	CAC	TTC	TTG	TCC	CAG	ACC	AAG	CAG	GCA	GGA	GAC	AAC	TTC		1776
5032	Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe		
5033				580					585					590				
5034																		
5035	CCC	TAC	CTG	GTA	GCA	TAC	CAA	GCC	ACG	GTG	TGC	GCC	AGG	GCT	CAG	GCC		1824

RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

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1998

5051 TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT
5052 Cys Met Ser Ala Asp Leu Glu Val Val Thr
5053 660 665
5054
5055
5056

6561 (2) INFORMATION FOR SEQ ID NO:111:

6562

6563 (i) SEQUENCE CHARACTERISTICS:

6564 (A) LENGTH: 2016 base pairs

6565 (B) TYPE: nucleic acid

6566 (C) STRANDEDNESS: single

6567 (D) TOPOLOGY: linear

6568

6569 (ii) MOLECULE TYPE: cDNA

6570

6571

6572 (ix) FEATURE:

6573 (A) NAME/KEY: CDS

6574 (B) LOCATION: 1..2016

6575

6576

6577 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

6578

6579 ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48

6580 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro

6581 1 5 10 15

6582

6583 CGC GGC AGC CAT ATG GCT TAC TCT CTG ACT ACG GGT TCT GTT GTT ATT 96

6584 Arg Gly Ser His Met Ala Tyr Ser Leu Thr Thr Gly Ser Val Val Ile

6585 20 25 30

6586

6587 GTT GGT AGA ATT ATT TTA TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC 144

6588 Val Gly Arg Ile Ile Leu Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser

6589 35 40 45

6590

6591 CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC 192

6592 Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly

6593 50 55 60

6594

6595 CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA 240

6596 Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr Ala

6597 65 70 75 80

6598

6599 ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT 288

6600 Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val

6601 85 90 95

6602

6603 TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC 336

6604 Tyr His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile

6605 100 105 110

6606

RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

DATE: 04/16/1999
TIME: 14:06:53

INPUT SET: S31474.raw

6607	ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG	384
6608	Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln Ala	
6609	115 120 125	
6610		
6611	CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC	432
6612	Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp	
6613	130 135 140	
6614		
6615	CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG	480
6616	Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg	
6617	145 150 155 160	
6618		
6619	GGC GAC AGT AGG GGG AGC CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG	528
6620	Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu	
6621	165 170 175	
6622		
6623	AAG GGC TCT GCT GGT GGT CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG	576
6624	Lys Gly Ser Ala Gly Gly Pro Leu Leu Cys Pro Ser Gly His Ala Val	
6625	180 185 190	
6626		
6627	GGC ATC TTC CGG GCT GCC GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG	624
6628	Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val	
6629	195 200 205	
6630		
6631	GAC TTT GTG CCC GTA GAG TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC	672
6632	Asp Phe Val Pro Val Glu Ser Met Glu Thr Thr Met Arg Ser Pro Val	
6633	210 215 220	
6634		
6635	TTC ACG GAC AAC TCA TCC CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG	720
6636	Phe Thr Asp Asn Ser Ser Pro Pro Ala Val Pro Gln Ser Phe Gln Val	
6637	225 230 235 240	
6638		
6639	GCC CAC CTA CAC GCT CCC ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG	768
6640	Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro	
6641	245 250 255	
6642		
6643	GCT GCA TAT GCA GCC CAA GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC	816
6644	Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser	
6645	260 265 270	
6646		
6647	GTT GCC GCT ACC TTA GGG TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT	864
6648	Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly	
6649	275 280 285	
6650		
6651	ATT GAC CCC AAC ATC AGA ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC	912
6652	Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ala	
6653	290 295 300	
6654		
6655	CCC GTC ACA TAC TCT ACC TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC	960
6656	Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys	
6657	305 310 315 320	
6658		
6659	TCT GGG GGC GCT TAT GAC ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT	1008

RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

DATE: 04/16/1999
TIME: 14:06:53

INPUT SET: S31474.raw

6660	Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr	
6661	325 330 335	
6662		
6663	GAC TCG ACT ACA ATC TTG GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG	1056
6664	Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu	
6665	340 345 350	
6666		
6667	ACG GCT GGA GCG CGG CTT GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA	1104
6668	Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly	
6669	355 360 365	
6670		
6671	TCG GTC ACC GTG CCA CAC CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT	1152
6672	Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Asn	
6673	370 375 380	
6674		
6675	ACT GGA GAG ATC CCC TTC TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC	1200
6676	Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile	
6677	385 390 395 400	
6678		
6679	AGG GGG GGA AGG CAT CTC ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC	1248
6680	Arg Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp	
6681	405 410 415	
6682		
6683	GAG CTC GCC GCA AAG CTG TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT	1296
6684	Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr	
6685	420 425 430	
6686		
6687	TAC CGG GGG CTC GAT GTG TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT	1344
6688	Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ile Gly Asp Val Val	
6689	435 440 445	
6690		
6691	GTC GTG GCA ACA GAC GCT CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC	1392
6692	Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp	
6693	450 455 460	
6694		
6695	TCA GTG ATC GAC TGT AAC ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC	1440
6696	Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser	
6697	465 470 475 480	
6698		
6699	TTG GAT CCC ACC TTC ACC ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA	1488
6700	Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Val Pro Gln Asp Ala	
6701	485 490 495	
6702		
6703	GTG TCG CGC TCG CAG CGG CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC	1536
6704	Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly	
6705	500 505 510	
6706		
6707	ATC TAC AGG TTT GTG ACT CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT	1584
6708	Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg Pro Ser Gly Met Phe Asp	
6709	515 520 525	
6710		
6711	TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG	1632
6712	Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu	

RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

DATE: 04/16/1999
TIME: 14:06:53

INPUT SET: S31474.raw

	530	535	540	
6713				
6714				
6715	CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA			1680
6716	Leu Thr Pro Ala Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr			
6717	545	550	555	560
6718				
6719	CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC			1728
6720	Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser Val			
6721		565	570	575
6722				
6723	TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG			1776
6724	Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys			
6725		580	585	590
6726				
6727	CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG			1824
6728	Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val			
6729		595	600	605
6730				
6731	TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG			1872
6732	Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys			
6733		610	615	620
6734				
6735	TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG			1920
6736	Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu			
6737		625	630	635
6738				640
6739	TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA			1968
6740	Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile			
6741		645	650	655
6742				
6743	ACC AAA TAC ATC ATG GCA TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT			2016
6744	Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val Thr			
6745		660	665	670
6746				
6747				
6748				
6749				
6750				

6751 (2) INFORMATION FOR SEQ ID NO:112:

6752

6753 (i) SEQUENCE CHARACTERISTICS:

6754 (A) LENGTH: 648 base pairs

6755 (B) TYPE: nucleic acid

6756 (C) STRANDEDNESS: single

6757 (D) TOPOLOGY: linear

6758

6759 (ii) MOLECULE TYPE: cDNA

6760

6761

6762 (ix) FEATURE:

6763 (A) NAME/KEY: CDS

6764 (B) LOCATION: 1..648

RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

DATE: 04/16/1999
TIME: 14:06:54

INPUT SET: S31474.raw

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6765
6766
6767      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:
6768
6769      ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG      48
6770      Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
6771      1              5              10              15
6772
6773      CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA      96
6774      Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
6775      20              25              30
6776
6777      TCT CCT GCT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT      144
6778      Ser Pro Ala Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu
6779      35              40              45
6780
6781      GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG      192
6782      Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu
6783      50              55              60
6784
6785      GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC      240
6786      Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr
6787      65              70              75              80
6788
6789      TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG      288
6790      Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys
6791      85              90              95
6792

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6793	ACC	TTA	GCC	GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT	GTG	336
6794	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	
6795				100					105						110		
6796																	
6797	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	TTG	384
6798	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	
6799				115				120					125				
6800																	
6801	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	CAT	432
6802	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	
6803				130				135					140				
6804																	
6805	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	CTG	480
6806	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	
6807	145					150					155					160	
6808																	
6809	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT	CCA	528
6810	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	
6811					165					170					175		
6812																	
6813	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	GTA	576
6814	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	
6815				180					185					190			
6816																	
6817	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	TCC	624

RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

DATE: 04/16/1999
TIME: 14:06:54

INPUT SET: S31474.raw

6818 Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser
6819 195 200 205
6820
6821 ATG GAA ACT ACT ATG CGG TCT TGA 648
6822 Met Glu Thr Thr Met Arg Ser
6823 210 215
6824
6825
6826

7236 (2) INFORMATION FOR SEQ ID NO:117:

7237

7238 (i) SEQUENCE CHARACTERISTICS:

7239 (A) LENGTH: 1941 base pairs

7240 (B) TYPE: nucleic acid

7241 (C) STRANDEDNESS: single

7242 (D) TOPOLOGY: linear

7243

7244 (ii) MOLECULE TYPE: cDNA

7245

7246

7247

7248 (ix) FEATURE:

7249 (A) NAME/KEY: CDS

7250 (B) LOCATION: 1..1941

7251

7252

7253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

7254

7255 ATG CAT ATG CAT CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG 48

7256 Met His Met His His His His His His His Leu Val Pro Arg Gly Ser Ala

7257 1 5 10 15

7258

7259 CCC ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC 96

7260 Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile

7261 20 25 30

7262

7263 AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT 144

7264 Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val

7265 35 40 45

7266

7267 CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC 192

7268 Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn

7269 50 55 60

7270

7271 GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC 240

7272 Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala

7273 65 70 75 80

7274

7275 GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC 288

7276 Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp

7277 85 90 95

7278

RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

DATE: 04/16/1999
TIME: 14:06:55

INPUT SET: S31474.raw

7279	CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC	336
7280	Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys	
7281	100 105 110	
7282		
7283	ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC	384
7284	Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val	
7285	115 120 125	
7286		
7287	ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG CTC TCC CCC	432
7288	Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro	
7289	130 135 140	
7290		
7291	AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA CTG CTC TGC	480
7292	Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Pro Leu Leu Cys	
7293	145 150 155 160	
7294		
7295	CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA TGC ACC CGG	528
7296	Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg	
7297	165 170 175	
7298		
7299	GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC ATG GAA ACT	576
7300	Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr	
7301	180 185 190	
7302		
7303	ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC CCC CCG GCC GTA	624
7304	Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val	
7305	195 200 205	
7306		
7307	CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC ACT GGC AGC GGC	672
7308	Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly	
7309	210 215 220	
7310		
7311	AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA GGG TAC AAG GTG	720
7312	Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val	
7313	225 230 235 240	
7314		
7315	CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG TTT GGG GCG TAT	768
7316	Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr	
7317	245 250 255	
7318		
7319	ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA ACT GGG GTA AGG	816
7320	Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg	
7321	260 265 270	
7322		
7323	ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC TAT GGC AAG TTT	864
7324	Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe	
7325	275 280 285	
7326		
7327	CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC ATC ATA ATA TGT	912
7328	Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys	
7329	290 295 300	
7330		
7331	GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG GGC ATC GGC ACA	960

RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

DATE: 04/16/1999
TIME: 14:06:55

INPUT SET: S31474.raw

7332	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	
7333	305					310					315					320	
7334																	
7335	GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	GTC	GTG	CTC	GCC	1008
7336	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	
7337					325					330					335		
7338																	
7339	ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	CCA	AAC	ATC	GAG	1056
7340	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	
7341				340					345					350			
7342																	
7343	GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC	TAT	GGC	AAA	GCC	1104
7344	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	
7345			355					360					365				
7346																	
7347	ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC	ATT	TTC	TGT	CAT	1152
7348	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	
7349		370					375					380					
7350																	
7351	TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	TCA	GGC	CTC	GGA	1200
7352	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly	
7353	385					390					395					400	
7354																	
7355	ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	TCC	GTC	ATA	CCA	1248
7356	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro	
7357				405					410					415			
7358																	
7359	ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	CTG	ATG	ACG	GGC	1296
7360	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly	
7361				420					425				430				
7362																	
7363	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC	ACA	TGT	GTC	ACC	1344
7364	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr	
7365			435					440					445				
7366																	
7367	CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC	ATT	GAG	ACG	ACG	1392
7368	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr	
7369		450					455					460					
7370																	
7371	ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG	CGG	GGT	AGG	ACT	1440
7372	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr	
7373	465					470					475					480	
7374																	
7375	GGC	AGG	GGT	AGG	AGA	GGC	ATC	TAC	AGG	TTT	GTG	ACT	CCG	GGA	GAA	CGG	1488
7376	Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg	
7377				485					490					495			
7378																	
7379	CCC	TCG	GGC	ATG	TTC	GAT	TCC	TCG	GTC	CTG	TGT	GAG	TGC	TAT	GAC	GCG	1536
7380	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala	
7381				500					505					510			
7382																	
7383	GGC	TGT	GCT	TGG	TAC	GAG	CTC	ACC	CCC	GCC	GAG	ACC	TCG	GTT	AGG	TTG	1584
7384	Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	Arg	Leu	

RAW SEQUENCE LISTING PATENT APPLICATION US/09/198,723A

DATE: 04/16/1999
TIME: 14:06:55

INPUT SET: S31474.raw

	515	520	525	
7385				
7386				
7387	CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG			1632
7388	Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu			
7389	530	535	540	
7390				
7391	GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC			1680
7392	Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His			
7393	545	550	555	560
7394				
7395	TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA			1728
7396	Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val			
7397		565	570	575
7398				
7399	GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA			1776
7400	Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser			
7401		580	585	590
7402				
7403	TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC			1824
7404	Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His			
7405		595	600	605
7406				
7407	GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC			1872
7408	Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val			
7409		610	615	620
7410				
7411	ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA TGC ATG TCG GCC			1920
7412	Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala			
7413		625	630	635
7414				640
7415	GAC CTG GAG GTC GTT ACG TAG			1941
7416	Asp Leu Glu Val Val Thr			
7417		645		
7418				
7419				
7420				

7974 (2) INFORMATION FOR SEQ ID NO:121:

7975

7976 (i) SEQUENCE CHARACTERISTICS:

7977 (A) LENGTH: 36 base pairs

7978 (B) TYPE: nucleic acid

7979 (C) STRANDEDNESS: single

7980 (D) TOPOLOGY: linear

7981

7982 (ii) MOLECULE TYPE: RNA (genomic)

7983

7984

7985

7986

7987 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

7988

7989 GCUCGCCCCGG GGAUCCUCUA GGAAUACACG UUCGAU 36

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/198,723A

DATE: 04/16/1999
TIME: 14:06:56

INPUT SET: S31474.raw

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